

from  
US 10/780,703-2.p2n.rmpm Seq Search Result

(Seq 3) does not  
encode Seq 2

RESULT 10  
US-10-780-703-3  
; Sequence 3, Application US/10780703  
; GENERAL INFORMATION:  
; APPLICANT: Lee, Jong Seob  
; APPLICANT: Kim, Yun Hee  
; APPLICANT: Choi, Eun kyung  
; APPLICANT: Yoo, So Yeon  
; APPLICANT: Ahn, Ji Hoon  
; APPLICANT: Choi, Yang Do  
; TITLE OF INVENTION: Gene Controlling Flowering Time of Plants and Method for  
; TITLE OF INVENTION: Manipulating Flowering Time of Plant Using the Same  
; FILE REFERENCE: 012679-105  
; CURRENT APPLICATION NUMBER: US/10/780,703  
; CURRENT FILING DATE: 2004-02-19  
; PRIOR APPLICATION NUMBER: KR 10-2003-10772  
; PRIOR FILING DATE: 2003-02-20  
; NUMBER OF SEQ ID NOS: 9  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO 3  
; LENGTH: 2606  
; TYPE: DNA  
; ORGANISM: Arabidopsis thaliana  
; FEATURE:  
; NAME/KEY: gene  
; LOCATION: (1)...(2606)  
; OTHER INFORMATION: genomic DNA of LOV1 gene  
US-10-780-703-3

## Alignment Scores:

Pred. No.:	1.24e-254	Length:	2606
Score:	1735.00	Matches:	378
Percent Similarity:	43.5%	Conservative:	0
Best Local Similarity:	43.5%	Mismatches:	1
Query Match:	85.3%	Indels:	490
DB:	61	Gaps:	3

US-10-780-703-2 (1-379) x US-10-780-703-3 (1-2606)

Qy	1 Met Ala Ile Val Ser Ser Thr Thr Ser Ile Ile Pro Met Ser Asn Gln Val Asn Asn Asn 20	
Db	1 ATGGCAATTGTATCCTCCACAACAAGCATCATTCCATGAGTAACCAAGTCAACAATAAC 60	
Qy	21 Glu Lys Gly Ile Glu Asp Asn Asp His Arg Gly Gly Gln Glu Ser His Val Gln Asn Glu 40	
Db	61 GAAAAAGGTATAGAACAAATGATCATAGAGGCGGCCAGAGAGTCATGTCCAAAATGAA 120	
Qy	41 Asp Glu Ala Asp Asp His Asp His Asp Met Val Met Pro Gly Phe Arg Phe His Pro Thr 60	
Db	121 GATGAAGCTGATGATCATGATCATGACATGGTCATGCCGGATTAGATTCCATCCTACC 180	
Qy	61 Glu Glu Glu Leu Ile Glu Phe Tyr Leu Arg Arg Lys Val Glu Gly Lys Arg Phe Asn Val 80	
Db	181 GAAGAAGAACTCATAGAGTTTACCTTCGCCGAAAAGTTGAAGGCAAACGCTTTAATGTA 240	
Qy	81 Glu Leu Ile Thr Phe Leu Asp Leu Tyr Arg Tyr Asp Pro Trp Glu Leu Pro ----- 97	
Db	241 GAACTCATCACTTCTCGATCTTATCGCTATGATCCTGGAACTTCCTGGTAAATAT 300	
Qy	97 ----- 97	

Db 301 ACATTCACATAAACACACATAAATCATCTCAAACATTTGGAAATCTTAATTCTATTCA 360  
 Qy 97 ----- 97  
 Db 361 TATGTTAAGATCTTCTCTCTCTTATCAGTTCTCTCTATTTCTTTTTAACCT 420  
 Qy 97 ----- 97  
 Db 421 ATATATGTACCTACCTCCTTATGAAGTATTACTATGTCATCGTTAACATTCTCAATAT 480  
 Qy 97 ----- 97  
 Db 481 CTTTAAACGCTCTCCCTCTTAGTTCTTAAACCTAACCTAACACCTACA 540  
 Qy 97 ----- 97  
 Db 541 TATATATCATAAGATATAAAATATGTGTATGTTTCATAATTAGCTTATGTATGTTAA 600  
 Qy 98 ----- AlaMetAlaAlaIleGlyGluLysGluTrpTyrPheTyr 110  
 Db 601 TCATAGATATATGTATATGCAGCTATGGCGCGATAGGAGAGAAAGAGTGGTACTTCTAT 660  
 Qy 111 ValProArgAspArgLysTyrArgAsnGlyAspArgProAsnArgValThrThrSerGly 130  
 Db 661 GTGCCAAGAGATCGGAAATATAGAAATGGAGATAGACCGAACCGAGTAACGACTTCAGGA 720  
 Qy 131 TyrTrpLysAlaThrGlyAlaAspArgMetIleArgSerGluThrSerArgProIleGly 150  
 Db 721 TATTGGAAAGCCACCGGAGCTGATAGGATGATCAGATGGAGACTTCTCGGCCTATCGGA 780  
 Qy 151 LeuLysLysThrLeuValPheTyrSerGlyLysAlaProLysGlyThrArgThrSerTrp 170  
 Db 781 TTAAAGAAAACCCTAGTTCTACTCTGGTAAAGCCCCTAAAGGCACTCGTACTAGTTGG 840  
 Qy 171 IleMetAsnGluTyrArgLeuProHisHisGluThrGluLysTyrGlnLysAla----- 188  
 Db 841 ATCATGAACGAGTATCGTCTCCGCACCATGAAACCGAGAAGTACCAAAAGGT-ATAAAAT 899  
 Qy 188 ----- 188  
 Db 900 TCTACTATAACTCTATATATCCTATTACATACATAGATATAACCTAGCTAGGTG 959  
 Qy 188 ----- 188  
 Db 960 GTGAGGCCTTAAATTGAAATTAAATCCCTAGACAGTTGAATTCTTTCTTTTGGACTA 1019  
 Qy 188 ----- 188  
 Db 1020 GTTTTATTTATTTATTTGGAATTGATTGATAAGATCAAAATACTTGTGAATGGACTA 1079  
 Qy 188 ----- 188  
 Db 1080 AATGTCAGGCAGCGTTGCGCTAAATCCAGAAAAATGTCATGTCATATGCGTGAACTC 1139  
 Qy 188 ----- 188  
 Db 1140 TTTAAATTGCTAGACATGGCCATATGTTATAGTAGAATACTTAAATAGATAGTCATA 1199  
 Qy 188 ----- 188  
 Db 1200 CACATATATATAAACACACAAAGTATCACACTCGACATTACACCTTAATTCTGCAGAG 1259

Qy	188	-----	188
Db	1260	ACATAGTTAGTTTCTTACAATTTGACATGAATGTTCTGCTCTTCCTCACATTAAT	1319
Qy	188	-----	188
Db	1320	TCATGTCTTCTATTTAAGTTACCCAACATTTTGAAATAATTGGCATATATGAATTAT	1379
Qy	188	-----	188
Db	1380	ACCAACATATTATATGCGAACATTTAAATCTATACGAATGATAACGGTTATGGAGTA	1439
Qy	188	-----	188
Db	1440	GACCGAAAAAATATTATGTATACGGAAAATGACAATGGATAGATAAAATACATTTTGGG	1499
Qy	188	-----	188
Db	1500	CTCTTCGACTTATATGTCGTACCCATTGAAACCATAAAATTATAAAATTCTATGTA	1559
Qy	188	-----	188
Db	1560	TATATATGATATTATGATGTATGCATAAGACAGCTAAAACAACAGGGTTGACATAATTAT	1619
Qy	188	-----	188
Db	1620	CTATGTGTATGTATTGCACATTCACTTGTACTAATAAAACTAAAATTACGCAATTAAATA	1679
Qy	188	-----	188
Db	1680	TATAAAAATAATAATATAATCATCTTAATTATTTGCATTGTTACGTATGATAG	1739
Qy	188	-----	188
Db	1740	TACTCTAAATTCTTCTAACGTGCTATCTTTTGCTAATGCTAACTTACATAGTT	1799
Qy	188	-----	188
Db	1800	GTGAATCTTCTTCAAAACCATATCTCGATAATGATATTTCATAGATATTGTTAGT	1859
Qy	188	-----	188
Db	1860	CTATATTGATAATTGATATATGTATCAAGTCTCTAATCAATGTGCTCATGTATAATT	1919
Qy	189	-----GluIleSerLeuCysArgValTyrLysArgProGlyValGluAspHisProSer	206
Db	1920	GluIleSerLeuCysArgValTyrLysArgProGlyValGluAspHisProSer	1979
Qy	207	TAGGCTGAAATATCATTGTGCCGAGTGTACAAAGGCCAGGAGTAGAAGATCATCCATCG	2039
Qy	227	207 ValProArgSerLeuSerThrArgHisHisAsnHisAsnSerSerThrSerArgLeu	226
Db	1980	207 ValProArgSerLeuSerThrArgHisHisAsnHisAsnSerSerThrSerArgLeu	2039
Qy	227	227 AlaLeuArgGlnGlnGlnHisHisSerSerSerAsnHisSerAspAsnAsnLeuAsn	246
Db	2040	227 AlaLeuArgGlnGlnGlnHisHisSerSerSerAsnHisSerAspAsnAsnLeuAsn	2099
Qy	247	247 AsnAsnAsnAsnIleAsnAsnLeuGluLysLeuSerThrGluTyrSerGlyAspGlySer	266
Db	2100	247 AsnAsnAsnAsnIleAsnAsnLeuGluLysLeuSerThrGluTyrSerGlyAspGlySer	2159

Qy 267 ThrThrThrThrThrAsnSerAsnSerAspValThrIleAlaLeuAlaAsnGlnAsn 286  
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||  
Db 2160 ACAACAAACAAACGACCACAAACAGTAACCTCTGACGTTACCATTGCTCTAGCCAATCAAAC 2219

Qy 287 IleTyrArgProMetProTyrAspThrSerAsnAsnThrLeuIleValSerThrArgAsn 306  
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||  
Db 2220 ATATATCGTCCAATGCCTTACGACACAAGCAACAAACACATTGATAGTCTCTACGAGAAAT 2279

Qy 307 HisGlnAspAspAspGluThrAlaIleValAspAspLeuGlnArgLeuValAsnTyrGln 326  
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||  
Db 2280 CATCAAGACGATGATGAAACTGCCATTGTTGACGATCTCAAAGACTAGTTAACTACCAA 2339

Qy 327 IleSerAspGly----- 330  
||| ||| |||  
Db 2340 ATATCAGATGGAGGTAACATCAATACCAATACTTCAAATTGCTAACAGTTCATCAT 2399

Qy 331 -----Ala 331  
|||  
Db 2400 ACTCAACAAACAAAATGCTAACGCAAACGCATTACAATTGGTGGCTGCAGCGACTACAGCG 2459

Qy 332 ThrThrLeuMetProGlnThrGlnAlaAlaLeuAlaMetAsnMetIleProAlaGlyThr 351  
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||  
Db 2460 ACAACGCTAACATGCCTCAAACCTCAAGCGCGTTAGCTATGAACATGATTCTGCAGGAACG 2519

Qy 352 IleProAsnAsnAlaLeuTrpAspMetTrpAsnProIleValProAspGlyAsnArgAsp 371  
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||  
Db 2520 ATTCCAAACAATGCTTGTGGATATGTGGAATCCAATAGTACCAAGATGGAAACAGAGAT 2579

Qy 372 HisTyrThrAsnIleProPheLys 379  
||| ||| |||  
Db 2580 CACTATACTAATATTCTTTAAG 2603